



SEQUENCE LISTING

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Pedersen, Sven
Svendsen, Allan

<120> Fungamyl-like Alpha-Amylase Variants

<130> 5835.200-US

<140> US 09/710,339

<141> 2000-11-09

<150> US 60/165,786

<151> 1999-11-16

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<170> PatentIn version 3.1

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<212> DNA

<213> Aspergillus Oryzae

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Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe
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Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr
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Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile
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atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat	344
Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp	
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gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac	392
Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn	
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Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu	
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Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr	
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Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser	
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Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp	
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Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu	
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Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile	
190 195 200 205	
gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa	776
Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys	
210 215 220	
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Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala	
225 230 235	
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Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro	
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Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met	
255 260 265	
gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac	968

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gct	tcg	ggt	gat	tcg	tat	acc	ctc	tcc	ttg	agt	ggt	gcg	ggt	tac	aca	1400	
Ala	Ser	Gly	Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala	Gly	Tyr	Thr		
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Ala	Gly	Gln	Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr	Val	Thr	Val		
ggt	tcg	gat	gga	aat	gtg	cct	ggt	cct	atg	gca	ggt	ggg	cta	cct	agg	1496	
Gly	Ser	Asp	Gly	Asn 450	Val	Pro	Val	Pro	Met	Ala	Gly	Gly	Leu	Pro	Arg		
gta	ttg	tat	ccg	act	gag	aag	ttg	gca	ggt	agc	aag	atc	tgt	agt	agc	1544	
Val	Leu	Tyr	Pro	Thr	Glu	Lys	Leu	Ala	Gly	Ser	Lys	Ile	Cys	Ser	Ser		
tcg	tgaagggtgg	agagtatatg	atggtactgc	tattcaatct	ggcattggac											1597	
Ser																	
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<212> PRT

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Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
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Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
80 85 90

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
95 100 105

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
110 115 120

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
125 130 135 140

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
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Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser

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165

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Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
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Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 205 210 215 220

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
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Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
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Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 255 260 265

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 270 275 280

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 285 290 295 300

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 305 310 315

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 320 325 330

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 335 340 345

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 350 355 360

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 365 370 375 380

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
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Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65 70 75 80

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
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Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
100 105 110

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
115 120 125

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
130 135 140

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145 150 155 160

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
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Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
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Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
195 200 205

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
210 215 220

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225 230 235 240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
245 250 255

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
260 265 270

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
275 280 285

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
290 295 300

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305 310 315 320

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala

325

330

335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
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Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
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Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
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Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
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Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
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Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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